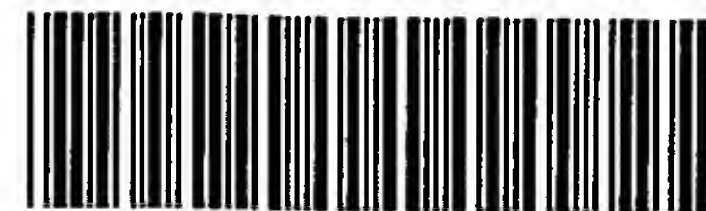


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The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/596,997
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TIME: 13:51:00

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5 <110> APPLICANT: Gillies, Stephen
6      Lo, Kin-Ming
7      Lan, Yan
8      Verma, Rakesh
10 <120> TITLE OF INVENTION: Compounds for Targeting
12 <130> FILE REFERENCE: ANTBH/P31763US
14 <140> CURRENT APPLICATION NUMBER: 10/596,997
15 <141> CURRENT FILING DATE: 2006-07-05
17 <150> PRIOR APPLICATION NUMBER: PCT/GB2005/000007
18 <151> PRIOR FILING DATE: 2005-01-05
20 <160> NUMBER OF SEQ ID NOS: 33
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 119
26 <212> TYPE: PRT
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: BC1 heavy chain variable region
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35 1          5          10          15
38 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
39          20          25          30
42 Val Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Leu
43          35          40          45
46 Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Gln Tyr Asn Glu Arg Phe
47          50          55          60
50 Lys Gly Arg Val Thr Met Thr Gly Asp Thr Ser Ile Ser Thr Ala Tyr
51 65          70          75          80
54 Met Glu Leu Ser Arg Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
55          85          90          95
58 Ala Arg Glu Val Tyr Gly Asn Tyr Ile Trp Gly Asn Trp Gly Gln Gly
59          100         105         110
62 Thr Leu Val Ser Val Ser Ser
63          115
66 <210> SEQ ID NO: 2
67 <211> LENGTH: 108
68 <212> TYPE: PRT
69 <213> ORGANISM: Artificial Sequence
71 <220> FEATURE:
72 <223> OTHER INFORMATION: BC1 light chain variable region
74 <400> SEQUENCE: 2
76 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly

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77 1          5          10          15
80 Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Ile Ser Ser Asn
81          20          25          30
84 Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
85          35          40          45
88 Ile Tyr Arg Thr Ser Asn Leu Ala Ser Gly Ile Pro Asp Arg Phe Ser
89          50          55          60
92 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
93 65          70          75          80
96 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Ser Ser Ile Pro
97          85          90          95
100 Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
101          100          105
104 <210> SEQ ID NO: 3
105 <211> LENGTH: 196
106 <212> TYPE: PRT
107 <213> ORGANISM: Artificial Sequence
109 <220> FEATURE:
110 <223> OTHER INFORMATION: IL-12p35 domain
112 <400> SEQUENCE: 3
114 Asn Leu Pro Val Ala Thr Pro Asp Pro Gly Met Phe Pro Cys Leu His
115 1          5          10          15
118 His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Met Leu Gln Lys Ala
119          20          25          30
122 Arg Gln Thr Leu Glu Phe Tyr Pro Cys Thr Ser Glu Glu Ile Asp His
123          35          40          45
126 Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro
127          50          55          60
130 Leu Glu Leu Thr Lys Asn Glu Ser Cys Leu Asn Ser Arg Glu Thr Ser
131 65          70          75          80
134 Phe Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met
135          85          90          95
138 Met Ala Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln
139          100          105          110
142 Val Glu Phe Lys Thr Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg
143          115          120          125
146 Gln Ile Phe Leu Asp Gln Asn Met Leu Ala Val Ile Asp Glu Leu Met
147          130          135          140
150 Gln Ala Leu Asn Phe Asn Ser Glu Thr Val Pro Gln Lys Ser Ser Leu
151 145          150          155          160
154 Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu
155          165          170          175
158 His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Val Met Ser Tyr
159          180          185          190
162 Leu Asn Ala Ser
163          195
166 <210> SEQ ID NO: 4
167 <211> LENGTH: 306
168 <212> TYPE: PRT

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169 <213> ORGANISM: Homo sapiens
171 <400> SEQUENCE: 4
173 Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp Trp Tyr
174 1          5          10          15
177 Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr Pro Glu
178          20          25          30
181 Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val Leu Gly
182          35          40          45
185 Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
186          50          55          60
189 Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Leu Leu
190 65          70          75          80
193 Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
194          85          90          95
197 Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala Lys
198          100         105         110
201 Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr
202          115         120         125
205 Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
206          130         135         140
209 Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val Arg Gly
210 145         150         155         160
213 Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala
214          165         170         175
217 Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala
218          180         185         190
221 Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg
222          195         200         205
225 Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu
226          210         215         220
229 Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp
230 225         230         235         240
233 Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln
234          245         250         255
237 Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp Lys Thr
238          260         265         270
241 Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg Ala
242          275         280         285
245 Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val Pro
246          290         295         300
249 Cys Ser
250 305
253 <210> SEQ ID NO: 5
254 <211> LENGTH: 8
255 <212> TYPE: PRT
256 <213> ORGANISM: Artificial Sequence
258 <220> FEATURE:
259 <223> OTHER INFORMATION: Mutated Linker Sequence
261 <400> SEQUENCE: 5

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263 Ala Thr Ala Thr Pro Gly Ala Ala
264 1 5
267 <210> SEQ ID NO: 6
268 <211> LENGTH: 646
269 <212> TYPE: PRT
270 <213> ORGANISM: Artificial Sequence
272 <220> FEATURE:
273 <223> OTHER INFORMATION: BC1 heavy chain fused to IL-12p35
275 <400> SEQUENCE: 6
277 Glu Val Gln Leu Val Gln Ser Gly Ala Asp Val Lys Lys Pro Gly Ala
278 1 5 10 15
281 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
282 20 25 30
285 Val Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Leu
286 35 40 45
289 Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Gln Tyr Asn Glu Arg Phe
290 50 55 60
293 Lys Gly Arg Val Thr Met Thr Gly Asp Thr Ser Ile Ser Thr Ala Tyr
294 65 70 75 80
297 Met Glu Leu Ser Arg Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
298 85 90 95
301 Ala Arg Glu Val Tyr Gly Asn Tyr Ile Trp Gly Asn Trp Gly Gln Gly
302 100 105 110
305 Thr Leu Val Ser Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
306 115 120 125
309 Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
310 130 135 140
313 Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
314 145 150 155 160
317 Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
318 165 170 175
321 Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
322 180 185 190
325 Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
326 195 200 205
329 Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
330 210 215 220
333 Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
334 225 230 235 240
337 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
338 245 250 255
341 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
342 260 265 270
345 Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
346 275 280 285
349 Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
350 290 295 300
353 Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
354 305 310 315 320

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357 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
358          325          330          335
361 Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
362          340          345          350
365 Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
366          355          360          365
369 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370          370          375          380
373 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
374 385          390          395          400
377 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
378          405          410          415
381 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
382          420          425          430
385 Ala Leu His Asn His Tyr Thr Gln Lys Ser Ala Thr Ala Thr Pro Gly
386          435          440          445
389 Ala Ala Asn Leu Pro Val Ala Thr Pro Asp Pro Gly Met Phe Pro Cys
390          450          455          460
393 Leu His His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Met Leu Gln
394 465          470          475          480
397 Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys Thr Ser Glu Glu Ile
398          485          490          495
401 Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys
402          500          505          510
405 Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys Leu Asn Ser Arg Glu
406          515          520          525
409 Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser
410          530          535          540
413 Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met
414 545          550          555          560
417 Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys Leu Leu Met Asp Pro
418          565          570          575
421 Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Ala Val Ile Asp Glu
422          580          585          590
425 Leu Met Gln Ala Leu Asn Phe Asn Ser Glu Thr Val Pro Gln Lys Ser
426          595          600          605
429 Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile
430          610          615          620
433 Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Val Met
434 625          630          635          640
437 Ser Tyr Leu Asn Ala Ser
438          645
441 <210> SEQ ID NO: 7
442 <211> LENGTH: 215
443 <212> TYPE: PRT
444 <213> ORGANISM: Artificial Sequence
446 <220> FEATURE:
447 <223> OTHER INFORMATION: BC1 light chain
449 <400> SEQUENCE: 7

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/596,997

DATE: 08/01/2006

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